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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                June 21, 2003, 19:16:44; Search time 1433 Seconds (without alignments) 214.734 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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17	17	17	17.4		17.4	
89.5	89.5	89.5	91.6	91.6	91.6	Query Match
772	250	187	1101	1039	522	Query Match Length DB
12	17	17	17	9	12	BB
BF627795	AZ083738	AZ248177	CNS04VNO	AU050798	BG347460	Length DB ID
BF627795 HVSMED000	AZ083738 RPCI-23-2	AZ248177 RPCI-23-3	AL309309 Tetraodon	AU050798 AU050798	BG347460 dab87all.	Description

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ALIGNMENTS

COMMENT	TITLE	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BG347460 LOCUS DEFINITION
Contact: Sandy Clifton, Ph.D. WashU Xenopus EST project, 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Library constructed by Life Technologies. DNA Sequencing by:	, Martin, J., Wylle, T., Underwood, K., Theising, B., Bowers, Y., Ferson, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R. WashU Xenopus EST project, 1999 Unpublished (1999)	Amphibia, Batrachia; Amura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopos. 1 (bases 1 to 522) Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.	BG347460.1 GI:13167884 BG347460.1 GI:13167884 EST. African clawed frog. African clawed frog.	BG347460 522 bp mRNA linear BST 28-FEB-2001 dab87ail.xl NICHD XGC Emb2 Xenopus laevis cDNA clone IMAGE:4404381 3' similar to SW:NOP4_YEAST P37838 NUCLEOLAR PROTEIN NOP4 ; mRNA

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14
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AUTHORS
TITLE
JOURNAL
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AU050798
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                                    339
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                            Contact: Takashi Aoki
Aguatic Biosciences
Tokyo University of Fisheries
Konan 4-5-7, Tokyo, Minato-ku 108-8477, Japan
Tel: 81-3-5463-0689
                                                                                                                                                                                                                                                                                                                                                                                                                      Paralichthys olivaceus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralichthyidae; Paralichthys.

(bases 1 to 1039)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU050798 naralichthys olivaceus library (Aoki olivaceus cDNA clone WHI1-23, mRNA sequence.
                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bastard halibut
                                                                                                                                                                                                                                                                       Email: aoki@tokyo-u-fish.ac.
clone WH11-23:similar to rat
                                                                                                                                                                                                                                                                                                                                                                                 Japanese flounder leukocyte cDNA
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU050798.1 GI:5019251
                                                                                                                                                                                                                                                                                                     Fax: 81-3-5463-0690
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                                    CGCTCTGAGTCCTGCTCTG
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/tissue_type="embryo, stage_17/19"
/lab_host="pH10B_(phage_resistant)"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
/noted_unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Life Technologies."

150 c 74 g 203 t
                                                                                                                                                /clone="WH11-23"
/clone lib="Paralichthys olivaceus library
/note="Organ: spleen"
/note="Organ: 47 t 10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Xenopus laevis"/db_xref="taxon:8355"
                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                  organism="Paralichthys olivaceus"
db_xref="taxon:8255"
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Pred. No. 1.8e+03;
0; Mismatches 1
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Pred.
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No. 2.3e+03;
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                                                                                                      Mus musculus
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Telraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNSO4VNO 1101 bp DNA linear (Tetraodon nigroviridis genome survey sequence T3 end 010F19 of library A from Tetraodon nigroviridis, genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGCTCTGATTCCTGCTCTG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is a single read and was generated as part of a lasscale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1101)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetie: Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL309309.1 GI:8216248
GSS; genome survey sequence.
Tetraodon nigroviridis.
Zhao,S., Nierman,W., Feldblyum,T.,
,B., Levins,M., Mcgann,S., Tsegaye,
and Fraser,C.M.
Mouse BAC End Sequences from Librar
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                                                                                             Bukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 187)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis DNA sequence
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324 c 294 g 211
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/db_xref="taxon:99883"
/clone="010F19"
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                                                                                                                                                                                                                                               GI:8561380
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                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 2.
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Mus
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                                          Iyum, T., Malek, J.,
Tsegaye, G., Geer, )
                                                                                                                                                                                                                                                                                                                 bp DNA linear GSS 15-JUN-2000 musculus genomic clone RPCI-23-39M14,
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                                                     Geer, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1101;
                                                                           Shatsman, S.,
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BASE COUNT
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                                                                                                                                                                                                                                                                                                     AUTHORS
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                                                               Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-22N10.TV
Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, U
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
17; Conser
Email: szhao@tigr.org
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23.
Clones are derived from the mouse BAC library RPCI-23.
                                                                                                                                                                                                                                                       Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong, P.
and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 250)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTCTGATTCCTGCTCT 43
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301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "30 c 65 g 34 t
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/clone="RPCI-23-39M14"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17; ; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 bp DNA linear GSS 08-MAY-2000 Mus musculus genomic clone RPCI-23-22N10,
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1 (bases 1 to 772)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex drought-stressed seedling shoot cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac ends/mouse/bac_end_intro.html plate: 22 row: N column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HVSMEb0005N04f Hordeum vulgare HVcDNA0002 (Dehydration stress)
HVSMEb0005N04f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
17; Conserv
                                                                                                                    Email: rwing@clemson.edu
Total hq bases = 131
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                              Clemson University
100 Jordan Hall, C
                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
On Dec 19, 2000 th
Contact: Wing RA
                                                                      High quality sequence stop: ?
Location/Qualifiers
                                                                                                                                                                                             Tel: 864 656 7288
Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                             Clemson University Genomics Institute
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/db_xref="taxon:10090"
/clone="RPCI-23~22N10"
                       organism="Hordeum vulgare"
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/sex="Female"
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cultivar="Morex"
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seedling shoot EST library
) Hordeum vulgare cDNA clone
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hes 0;
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288 CTCTGATTCCTGCTCTG 272
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oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site
                                                                                                                                                                            University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 256)
Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
                                                                                                                                                                                                                                                                                                              Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                              discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI293206.1 GI:14954485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Norway rat
                                                                                                           The sequence contained an oligo-dT track that was present in the
                                                                                                                                            Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda-gov/ggpages/bgn/31/cover.html)" a 140 c 229 g 109 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 90% RH for 24 hr. Shoots were then harvested
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence analysis see
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HVcDNAO002 (Dehydration stress)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="Seedling shoot"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="HVSMEb0005N04f"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No. 3.1e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                  188
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                                                                                                         AA884860 259 bp mRNA linear EST 27-MAK-1990
am21b02.sl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1467435 3' similar to TR:Q91638 Q91638 TAIL-SPECIFIC THYROID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GCTCTGATTCCTGCTCTG
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AA884860.1
                                                                               HORMONE UP-REGULATED ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCTGTTTCCTGCTCTG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               individually according to the procedure described by Bonaldo, Lemmon & Soares (Genome Research Genome 6: 791-806, 1996). For construction of the DKO subtracted library, plasmid DNA from each of the five individually tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria for production of single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing these five normalized libraries was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA template preparation) comprising: a) a set of about 1,000 arrayed clones from each of the five norm-lormalized libraries of brain (CTOs), heart (CSOs), kidney (CUOs), aorta (CWOs), and placenta (CXOs). The resulting pool of approximately 5,000 clones represented about 2,000 arrayed clones from each of the five normalized ilbraries of brain (CTOs), heart (CSO), kidney (CUO), aorta (CWO), and placenta (CXO). The resulting pool of about 3.3% of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized ilbraries of brain (CTOs), heart (CSO), kidney (CUO), aorta (CWO), and placenta (CXO). The resulting pool of about 10,000 clones represented about 50,000 clones from set of set the final driver normalized the represented about 66 of the final driver normalized clones represented about 66 of the final driver normalized clones represented about 66 of the final driver normalized clones represented about 66 of the final driver normalized clones represented about 66 of the final driver normalized clones represented about 66 of the final driver normalized clones represented about 66 of the final driver normalized clones represented about 66 of the final driver normalized clones represented about 66 of the final driver normalized clones represented about 66 of the final driver normalized clones represented about 66 of the final driver normalized clones final driver normalized clones final drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_SEQ=ATAAGATAAC"
1 36 c 92 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_LIB=UI-R-DK0
TAG_TISSUE=rat heart
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db_xref="taxon:10116"
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Pred. No. 3.9e+03;
                                                                                        mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 GCTCTGATTACTGCTCTG
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                         BF551260 267 bp mRNJ
UI-R-CO-ig-e-05-0-UI.r1 UI-R-CO Rattus
UI-R-CO-ig-e-05-0-UI 5', mRNA sequence
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High quality sequence stop: 1.
    Location/Qualifiers
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1 (bases 1 to 259)
                                                                                                                                                                                                                                                                                                                                                                                        BF551260
BF551260.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                    Genome Res. 6 (9),
                                                                                                                                                                                                                  1 (bases 1 to 267)
Bqnaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                   97044477
                                                                                                                                                                                              Normalization and subtraction:
                                                                                                                                                                                                                                                              Rattus.
                                                                                                                                                                                                                                                                                                                                               Norway rat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'clone="IMAGE:1467435"
'clone lib="Soares_NFL_T_GBC_S1"
'lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.3%;
                                                                                                                                                                                                                  Lennon, G. and Soares, M.B
                                                                                                                                                       791-806 (1996)
                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.4; DB 9;
Pred. No. 4e+03;
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                                                                                                                                                                                            two approaches to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         m.R.N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A linear EST 12-DEC-2000 norvegicus cDNA clone
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RESULT 10
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cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1774202
Seg primer: Mi3 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TaE05017F05F TaE05 Triticum aestivum cDNA clone TaE05017F05F, mRNA
Cereal Research Centre, Agriculture and Agri-food Canada 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
                                                                    Unpublished (2002)
Contact: Dr. Sylvie Cloutier
                                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta; ; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                               Triticum aestivum
                                                                                                                                            Wheat functional genomics -
                                                                                                                                                                                Cloutier,S.
                                                                                                                                                                                                                                                                                                                                                                                       bread wheat
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//lab host="Mallos (Life Technologies)"
//lab host="Mallos (Life Technologies)
//lab host="Mallos (Life Techn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single-stranded circles. The remaining single-stranded
circles (subtracted library) was purified by
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/clone="UI-R-CO-ig-e-05-0-UI"
/clone_lib="UI-R-CO"
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94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 318)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasmid inserts
Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                             High
                                                                                                                                                                                                           Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0004 row: J column: 11
                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                             quality sequence stop: 318.
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/dev_stage="5 days after anthesis"
/lab_host="5. coli DH108"
/note="Vector: pSPORT-P (Invitrogen Technologies); Site_1:
NotI; Site_2: MluI; mRNA obtained from wheat seeds of
cultivar GTenlea 5 days post-anthesis"
a 67 c 109 g 66 t
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|cultivar="Glenlea"
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/clone="TaE05017F05F"
/clone="UUGC2M0004J11"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                          organism="Mus musculus"
                                                                                                                                        Location/Qualifiers
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                                               db_xref="taxon:10090"
                                                                       strain="C57BL/6J"
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nes 17; Conserv
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Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci (Sonno, H., Aizawa, K., Fukunishi, Y., Hara, A., Hayatsu, N., P., Endo, T., Fukuda, S., Fukunishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Hirozane, T., Kori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shijemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suyahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Watanabe, S., Yamamura, T., Yamanaka, I., K., Muramatsu, M. and Hayashizaki, Y., Soshida, K., Yoshiki, A., Yoshino, R., Kasumatsu, M., and Hayashizaki, Y., Rakai, C., Kananaka, I., Kolon, H., et al.)
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Carninci, P., Nishiyama, Y., Westöver, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Centear(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jag Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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                                                                                                                                                                        Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                    81-45-503-9216
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:8780123
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94.4%;
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Pred. No. 4.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 17;
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                                                                                                                       TITLE
                                                                                                                                                                                                                                                          AUTHORS
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                                                                                                                                  Dias Neto,E., Garcia Correa,R., verjovshi-hamman, ..., ..., ..., Ragai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Magai,M.A., Baia,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GCTCTGATTCCTGCTCTG 19
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PM0-HT0913-150201-006-h07 HT0913 Homo sapiens cDNA, BG994801
                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                     human.
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                                                                      Proc. Natl. Acad. Sci. U.S.A. 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTATGATTCCTGCTCTG 156
                                                                                                                                                                                                                                            (bases 1 to 353)
as Neto,E., Garcia Correa,R., Verjovski-Almeida,S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genômic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGCCAAGAGCTCTTTTTTTTTTTTTTTYN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper, cDNA went through one round of normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="cerebellum"
/dev_stage="16 days neonate"
/lab_host="DH103"
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clone="9630008M03"
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94.4%;
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Pred. No. 4.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following UKL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM0kt2=PM0-HT0913-150201-006-h07kt3=2001-02-15kt4=1)
                                                                                                                                                                                                                                               Harvard Medical School
75 Francis St. Boston, MA 02115,
                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 364)
Liew,C.C., Hwang,D.M., Fung,Y.W., Laurenssen,C., Cukerman,E.,
,S. and Lee,C.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A1480F Heart Homo sapiens cDNA clone A1480, T11530
                                                                                                                                                                               Seq primer: GGTGGCGACGACTCCTGGAGCC.
                                                                                                                                                                                                                                                                                 Brigham and Women's Hospital
                                                                                                                                                                                                                                                                                                    Contact: Liew CC
                                                                                                                                                                                                                                                                                                                        95024171
                                                                                                                                                                                                                                                                                                                                                      expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                     A catalogue of genes in the cardiovascular system as identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ludwig Institute for Cancer Research
                                                                                                                                                                                             Email: cliew@rics.bwh.harvard.edu
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/clone_lib="Heart"
/clone_lib="Cooli Y1090"
/lab host="E.coli Y1090"
/note="Yector: Lambda gtl1; Site_1: EcoRI; Site_2: EcoRI"
/note="Yector 46 q 86 t
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                                                                                                            db xref="taxon:9606"
                                                                                                                             organism="Homo sapiens"
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Pred. No. 4.4e+03;
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39
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Nagai,M.A., da Silva,W. Jr., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brumstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGCTCTGATTCCTGCTCT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF086663 392 bp mRNA linear EST 19-OCT-2000 CM0-GN0079-150900-547-d04 GN0079 Homo sapiens cDNA, mRNA sequence.
                                                                                     l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq primer: puc 18 forward
High quality sequence start: 39
High quality sequence stop: 392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMO-GN0079-150
900-547-d04&t3=2000-09-15&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simpson, A.\,\mathrm{J}. Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF086663.1 GI:10892373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CECTCTGATTCCAGCTCT 112
GCTCTGATTCCAGCTCTG 22
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                                                                                     Conservative
                                                                                                                                                                                                    91
                                                                                                                                                                                        /note="Organ: placenta_normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORSSTES PCR (U.S. Letters Pattent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"

db_xref="taxon:9606"

clone_lib="GN0079"
                                                                                                                                                                                                                                                                                                                                                                                   dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.3%;
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                                                                                     0;
                                                                                  Score 16.4; DB 12;
Pred. No. 4.5e+03;
0; Mismatches 1;
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Search completed: June 21, 2003, 20:20:28
Job time: 1437 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 1.0
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19
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230.422 Million cell updates/sec
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/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	œ	7	ማ	ຫ	4.	w	2	щ	Result
16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	Score
86.3		86.3	86.3	86.3	86.3	86.3	86.3	86.3	86.3	86.3	86.3	86.3	86.3	86.3	86.3	86.3	86.3	86.3	Query Match
2550	2550	2550	2550	2550	2550	2550	2550	2550	2550	2550	2550	2550	2550	2550	2550	2550	2550	1769	Length
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US-10-143-032-59	US-10-141-755-59	US-10-121-050-59	US-10-142-423-59	US-10-123-262-59	US-10-142-419-59	US-10-140-002-59	US-10-143-114-59	US-10-142-431-59	US-10-140-474-59	US-10-137-865-59	US-10-176-921-59	LO-176-918-5	US-10-175-746-59	US-10-140-470-59	US-10-123-904-59	US-10-121-049-59	US-10-028-072-59	US-09-728-952-95	ID
Sequence 59, Appl	Sequence 59, Appl	Sequence 59, Appl			-	-	59,		59,	59,	Sequence 59, Appl	•	•	•	•	Sequence 59, Appl	Sequence 59, Appl	Sequence 95, Appl	Description

45	44	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20
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0-127-825A-	-10-125-924-5	0-125-922-5	-10-124-824-5	-10-124-817-5	0-124-813-5	-10-123-910-5	-10-123-909-5	-10-123-908-5	- 1	-10-123-215-5	-10-121-047-5	-10-121-043-5	-10-121-041-5	-10-160-498-5	-10-140-925-5	-10-124-822-5	0-124-819-5	-10-123-903-5	-10-123-292-5	0-121-045-5	-10-140-928-	-10-140-921-5	-10-123-261-	0-123-236-5	-108-
equence 5	ω ω	equence 5	equence 5	nce E	equence 5	Sequence 59	equence 5	equence 5	Sequence 59	equence 5	(D	(D	(D	(D	in	(D	(D	(D UT	equence 5	o u	6 5	Sequence 59	o U	Sequence 59,	Sequence 59
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ALIGNMENTS

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APPLICANT: Drmanac, Radoje T.

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. US20020111302A1el Nucleic Acids and

TITLE OF INVENTION: Polypeptides

FILE REPERENCE: 799

CURRENT APPLICATION NUMBER: US/09/728,952

CURRENT FILING DATE: 2000-11-30

NUMBER OF SEQ ID NOS: 101

SOFTWARE: pt FL_genes Version 2.0

SEQ ID NO 95

LENGTH: 1769

TYPE: UNA

ORGANISM: Homo sapiens

FRATURE:

NAME/KEY: CDS

LOCATION: (282)...(1769)

US-09-728-952-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
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RESULT 2
US-10-028-072-59
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Patent No. US20020111302A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                   Matches 17; Conservative
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APPLICANT:
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Best Local Similarity
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Zhou, Ping
Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
Wang, Jian-Rui
Wang, Dunrui
Yamazaki, Vicki
Ujwal, Manusha L.
                                                                                                                                  86.3%; Score 16.4; I
94.4%; Pred. No. 80;
tive 0; Mismatches
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                                                                                                                                     0
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1997-11-07

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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laureen
APPLICANT: DeForge, Laureen
APPLICANT: DeForge, Laureen
APPLICANT: DeForge, Laureen
APPLICANT: Filvaroff, Filen
APPLICANT: Gao, Wei-Oiang
APPLICANT: Gao, Wei-Oiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: ALANG
TILLE REFERENCE:
TILE REFERENCE:
TILE REFERENCE:
FILLE REFERENCE:
FILLE APPLICATION NUMBER: US/10/028,072
CURRENT FILLING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/05911
PRIOR FILLING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/05911
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
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PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059122
PRIOR APPLICATION NUMBER: 60/059122
PRIOR APPLICATION NUMBER: 60/059124
PRIOR APPLICATION NUMBER: 60/059125
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PRIOR FILLING DATE: 1997-09-24
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Publication No. US20030004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062285
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062287
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062814
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/062816
OR APPLICATION NUMBER: 60/062816
                                                        FILING DATE: 1997-10-27
APPLICATION NUMBER: 60/063550
FILING DATE: 1997-10-28
APPLICATION NUMBER: 60/063561
FILING DATE: 1997-10-28
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FILING DATE: 1997-10-31
APPLICATION NUMBER: 60/063127
FILING DATE: 1997-10-24
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APPLICATION NUMBER: 60/063045
FILING DATE: 1997-10-24
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FILING DATE: 1997-10-27
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                            APPLICATION NUMBER: 60/063704
      1997-10-29
                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1998-02-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165
PRIOR APPLICATION NUMBER: 60/080165
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR PRIOR APPLICATION NUMBER: 60/081695
PRIOR APPLICATION NUMBER: 60/081695
PRIOR FILING DATE: 1998-04-14
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR APPLICATION NUMBER: 60/081817
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OR APPLICATION NUMBER: 60/069212
OR FILING DATE: 1997-12-11
OR APPLICATION NUMBER: 60/069278
OR FILING DATE: 1997-12-11
OR APPLICATION NUMBER: 60/069334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OR APPLICATION NUMBER: 60/077791
OR FILLING DATE: 1998-03-12
OR FILLING DATE: 1998-03-20
OR FILLING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/079294
OR FILLING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079663
OR APPLICATION NUMBER: 60/079663
OR FILING DATE: 1998-02-27
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FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/064248
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APPLICATION NUMBER: 60/063735
FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063738
FILING DATE: 1997-10-29
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APPLICATION NUMBER: 60/066364
FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/066453
FILING DATE: 1997-11-24
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APPLICATION NUMBER: 60/069694
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FILING DATE: 1997-11-24
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APPLICATION NUMBER: 60/064809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/073612
FILING DATE: 1998-02-04
APPLICATION NUMBER: 60/074086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/072320 FILING DATE: 1998-01-23
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084627
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084637
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FILING DATE: 1998-04-24
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APPLICATION NUMBER: 60/074092
FILING DATE: 1998-02-09
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                                                                                                                    APPLICATION NUMBER: 60/084600
                                                                                                                                                APPLICATION NUMBER: 60/083545
FILING DATE: 1998-04-29
                                                                                                                                                                                                               FILING DATE: 1998-04-28
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1997-12-16

FILING DATE: APPLICATION 1

NUMBER: 60/084637 : 1998-05-07

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US-10-121-049-59
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Best Local S
Matches 17
                                                                  Sequence 59, Application US/10121049 Publication No. US20030022239A1 GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maur
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
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FILING DATE: 19/98-06-11
APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-10
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/085704
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/086414
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085697
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
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APPLICATION NUMBER: 60/085339
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APPLICATION NUMBER: 60/091360
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APPLICATION NUMBER: 60/089947
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17; Conserv
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              Beresini, Maureen
DeForge, Laura
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Pred. No. 80;
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                                                                ; SEQ ID NO 59
; LENCTH: 2550
; TYPE: DNA
; ORGANISM: Homo S
US-10-123-904-59
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; ORGANISM: Homo Sapien
US-10-121-049-59
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US-10-123-904-59
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SEQ ID NO 59
LENGTH: 2550
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRAME POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FAPILICATION NUMBER: US/10/121,049
Prior Application removed - See File Wrapper or Palm
                                                                                                                                                    Prior Application removed - NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
                                                                                                                                                                                                                        APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
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17; Conserv
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Godowski, Paul J.
Gurney, Austin L.
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Gurney, Austin L.
Sherwood, Steven
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Watanabe, Colin K
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Wood, William
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Gao, Wei-Qiang
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to. US20030022328A1
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Conservative
              94.4%;
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              Score 16.4;
Pred. No. 8
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Pred. No. 80;
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; LENGTH: 2550
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US-10-140-470-59
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US-10-175-746-59
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maur
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Best Local Similarity
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330RIC160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
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APPLICANT: Zhang, L
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                           Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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                              Tumas, Daniel
Watanabe, Colin K
Wood, William
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Wood, William
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                                                                             Stewart, Timothy A
                                                                                                                                                                            Gerritsen, Mary E
                                                                                                                                                                                          Gao, Wei-Qiang
                                                                                                                                                                                                            Filvaroff, Ellen
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                                                                                               Smith, Victoria
 SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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94.4%;
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Pred. No. 80;
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US-10-176-921-59

Sequence 59, Application US/10176921 Publication No. US20030027276A1 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maur APPLICANT: DeForge, Laura

Beresini, Maureen DeForge, Laura

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFRENCE: 93330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 59
; SEQ ID NO 59
; ENGTH: 2550
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RESULT 8
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                                                                                                                                                                                                              TITLE OF INVENTION: SECRETED AND TRANSMEMERANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P330R1C382
CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
SEQ ID NO 59
LENGTH: 2550
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Best Local
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Best Local :
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                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo Sapien
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17; Conserv
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                                               GCTCTGATTACTGCTCTG 455
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Wood, William
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                                                                                                                        86.3%;
94.4%;
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94.4%;
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                                                                                                       ; Score 16.4;
; Pred. No. 80
0; Mismatche
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Pred. No. 80;
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; TYPE: DNA; ORGANISM: Homo Sapien US-10-176-921-59
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 59
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Matches 17; Conservative
                                                                                              SEQ ID NO 59
LENGTH: 2550
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Publication No.
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Best Local Similarity
                 Query Match
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CURRENT APPLICATION NUMBER: US/10/176,921
CURRENT FILING DATE: 2002-06-20
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TITLE OF INVENTION: SECRETED AND TRANSMEMERANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACCIDS ENCODING THE SAME
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                                                                                                                             TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R10154
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER: OF SEQ ID NOS: 550
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APPLICANT: Beresini, Maur
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                                                                 TYPE: DNA ORGANISM: Homo Sapien
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Watanabe, Colin K
Wood, William
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Filvaroff, Ellen
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Wood, William
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Filvaroff, Ellen
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Gurney, Austin L.
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86.3%;
94.4%;
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Pred. No. 80;
Score 16.4; 1
Pred. No. 80;
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US-10-140-474-59
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; ORGANISM: Homo Sapien
US-10-140-474-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 59
LENGTH: 2550
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Best Local
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CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or F.
NUMBER OF SEQ ID NOS: 550
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                    Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Watanabe, Colin K
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to. US20030032156A1
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Gerritsen, Mary E.
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Zhang, Zemin
               Watanabe, Colin K
Wood, William
                                             Tumas,Daniel
                                                      Stewart, Timothy A.
                                                                        Smith, Victoria
                                                                                                                                Goddard, Audrey
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Filvaroff, Ellen
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Pred. No. 8
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Mismatches
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; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-142-431-59
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US-10-143-114-59
                                                                               US-10-140-002-59
                                                                                                 RESULT 13
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 59
LENGTH: 2550
             Sequence 59, Application US/10140002
Publication No. US20030037623A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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Best Local Similarity
                                                                                                                                                                                                                                     Best
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LENGTH: 2550
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                 Query Match
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CURRENT APPLICATION NUMBER: US/10/142,431
CURRENT FILING DATE: 2002-05-10
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                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/143,114
CURRENT FILING DATE: 2002-05-09
Prior Application removed - See Palm or FINMBER OF SEQ ID NOS: 550
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APPLICANT:
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                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                    Local Similarity
nes 17; Conserv
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Beresini, Maureen
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No. US20030036180A1
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Wood,William
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DeForge,Laura
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Gurney, Austin L.
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Pred. No. 80;
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US-10-142-419-59
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LENGTH: 2550
TYPE: DNA
ORGANISM: Homo Sapien
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Publication No. US20030044945A1
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CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
Query Match
                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333081C244
CURRENT APPLICATION NUMBER: US/10/142,419
CURRENT FILING DATE: 2002-05-10
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                                                                                                               Prior Apploication removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
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                                                TYPE: DNA
ORGANISM: Homo
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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Godowski, Paul
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Filvaroff,Ellen
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Gerritsen, Mary E.
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94.4%; Pred. No. 80;
tive 0; Mismatches
 86.3%;
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APPLICANT: Stewart, Finothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zharg, Zemin
FITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REPERENCE: P3330R1C38
CURRENT APPLICATION NUMBER: US/10/123,262
CURRENT FILING DATE: 2002-04-15
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 59
LENGTH: 2550
TYPE: DNA
ORGANISM: Homo Sapien
US-10-123-262-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 59, Application US/10123262
Publication No. US20030049816A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DePorge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
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US-10-123-262-59
Search completed: June 21, 2003, 21:12:24
Job time : 122 secs
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Goddowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Maximum Match 100%
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1: /cgn2_6/pcodata/2.

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5: /cgn2_6/ptodata/2.

6: /cgn2_6/ptodata/2.
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Match Length
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-096-623A-19
US-09-443-501A-2
US-08-724-394A-21
US-08-724-394A-21
US-08-724-394A-22
US-08-724-394A-22
US-08-724-394A-22
US-08-724-394A-22
US-08-724-394A-22
US-08-129-129-7
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US-09-514-247A-9
US-09-514-247A-9
US-09-611-781-7
US-09-611-781-7
US-09-611-781-1
US-09-298-358-1
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Sequence 19, Appli
Sequence 20, Appli
Sequence 21, Appli
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Sequence 25, Appli
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Sequence 11, Appli
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Sequence 1, Appli
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Patent No. 5
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APPLICANT: Proffitt, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yen, Huei-Che B.
TITLE OF INVENTION: Biosynthesis
TITLE OF INVENTION: Glycosylated

104

of Zeaxanthin and Zeaxanthin in Genetically Engineered Hosts

Brinkhaus, Friedhelm I Mukharji, Indrani Proffitt, John H. Yarger, James G. Yen, Huei-Che B.

APPLICANT: Ausich,
APPLICANT: Brinkhau
APPLICANT: Mukharj

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INFORMATION:

), Application US/08096623A 5684238

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US-09-058-389A-5 US-09-611-781-5 US-08-665-259-19 US-08-762-500-19 US-08-955-138-1 US-07-925-695-2 US-08-770-379-20 US-08-770-379-20 US-08-770-3714A-21 US-09-230-371A-21 US-09-230-371A-21 US-08-808-81-11 US-09-107-631-11 US-08-808-81-11	j-4	μ.	4	υī	μ	w	W	4.	4,	N	ш	μ	N	ω	w	4	w	
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ALIGNMENTS

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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/096,623A
FILING DATE: 22-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
PRIOR APPLICATION NUMBER: US 07/662,921
FILING DATE: 03-DATA:
APPLICATION NUMBER: US 07/562,674
FILING DATE: 03-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/525,551
FILING DATE: 18-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,613
APPLICATION NUMBER: US 07/487,613
APPLICATION NUMBER: US 07/487,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                          FILING DATE: 02-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 S. Riverside Plaza, 22nd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicago
:: IL
TRY: USA
                                             29,381
                          AMO-006.1
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US-09-443-501A-2/c
US-09-443-501A-2/c
; Sequence 2, Application US/09443501A
; Patent No. 6303342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: DNA (genom.; POSITION IN GENOME: MAP POSITION: 1 to 1200 UNITS: bp US-08-096-623A-19
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; Sequence 20, Applicatic
; Patent No. 5872237
; GENERAL INFORMATION:
APPLICANT: Feder, J
APPLICANT: Kronmal,
                                                                                      US-08-724-394A-20
                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic construct US-09-443-501A-2
                                                                                                        RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/130,560
PRIOR PILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: US 60/122,620
PRIOR FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: US 60/119,386
PRIOR FILING DATE: 1999-02-10
PRIOR PILING DATE: 1998-11-20
PRIOR FILING DATE: 1998-11-20
                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Recombinant Methods and Materials for Producing TITLE OF INVENTION: Epothilone and Epothilone Derivatives FILE REFERENCE: 30062-20031.00 CURRENT APPLICATION NUMBER: US/09/443,501A CURRENT FILING DATE: 1999-11-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (312) 655-1501
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kosan Biosciences,
APPLICANT: Julien, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                               LENGTH: 71989
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 17; Conserv
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                                                                                                                                                          63977 CGCTCTGATTCCAGATCTG 63959
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                                                     0, Application US/08724394A
5872237
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Katz, Leonard
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Feder, John N.
Kronmal, Gregory S.
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Pred. No. 64;
                                                                                                                                                                                                                              Score 15.8; DB of Pred. No. 1e+02; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                                               Patent No. 5872237
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity Matches 17; Conserv
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Best Local
                                                                                                                                                                                                                                                                                                  Sequence 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0)
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,
                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                  NUMBER OF SEQUENCES:
                                                                                                   TITLE OF INVENTION: Megabase Transcript Map: No. 58
                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                        161737 cecrcicarieciecicie 161755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..24624
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1..246240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGCTCTGATTCCTGCTCTG 19
San Francisco
CA
                                                                                                                                                                                                                                                                                                Application US/08724394A
                                                                                                                                                      Lauer, Peter M.
Ruddy, David A.
Thomas, Winston
Tsuchihashi, Zenta
                                                                                                                                       Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                              Feder, John N.
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Pred. No. 1
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1.1e+02;
2;
                                                                                                                         No. 5872237e3
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INFORMATION FOR SEQ ID NO: 21:
                                                                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWAPER: PAT-TT Pa-255-410
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REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fitts, Renee A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Megabase Transcript Map: No. 58
                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CITY: San Francisco
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                                                APPLICATION NUMBER: US/08/724,394A FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                   ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor
                                    CLASSIFICATION:
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Wolff, Roger K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feder, John N.
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Pred. No. 1.1e
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Query Match
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US-08-592-126-95/c
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US-08-592-126-95
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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             ORIGINAL SOURCE: INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                             TOPOLOGY: li
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                                              ANTI-SENSE:
                                                             HYPOTHETICAL:
                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                   SLECUPALLE (ALL.)
TELEPHONE: (ALL.)
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SOFTWARE: Patentin Palaring Patentin Palaring Patentin Palaring
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OTHER INFORMATION: /note= "HLA-H.CONTIG"
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LOCATION: 1..246240
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                                                                                                                                                                                                                                        NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
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350 Cambridge Avenue, Suite 250
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Pred. No. 1.1e+02;
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                                                                                                                   Sequence 11, Application US/08139937 Patent No. 5821070
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Best Local Similarity
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                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/923,137
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,700
FILING DATE: 06-SEP-1996
ATTORNEY_AGENT INFORMATION:
NAME: Bak, Wary E.
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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REFERENCE/DOCKET NUMBER: GNT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
TYPE: Floppy disk
                               APPLICANT: SHAN, BET
TITLE OF INVENTION: CELLULAR GENES ENCODING
TITLE OF INVENTION: RETINOELASTOMA-ASSOCIATED PROTEINS
                                                                   APPLICANT:
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 CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 36519 base pairs
TYPE: nucleic acid
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OF SEQUENCES: 1
PONDENCE ADDRESS:
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                                                                                   LEE, WEN-HWA
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Steven F.
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                                                                                                                                                                                                                                                                                        81.1%; Score 15.4; DB 3;
94.1%; Pred. No. 1.5e+02;
tive 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                        Length 36519;
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; TOPOLOGY: linear; MOLECULE TYPE: CDNA. US-08-139-937-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application PC/TUS9311310 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 20-OCT-1993
CLASSIFICATION: 43
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/979,156
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CJ 9370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 619-535-900
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO:
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
NATIONAL MEDICAL NATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/139,937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BOARD OF REGENTS OF THE UNIVERSITY OF TEXAS SYSTEM TITLE OF INVENTION: CELLULAR GENES ENCODING TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS
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NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: FP-CJ 9790
TELECOMMUNICATION INFORMATION:
                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Pelacet
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CITY: SAN DIEGO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 92122
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                                                                                                FILING DATE: 1:
CLASSIFICATION:
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                                                                                                                    APPLICATION NUMBER: PCT/
FILING DATE: 19-NOV-1993
                                                                                                                                                                                                                                                                                                                                           CITY: SAN DIEGO
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                                                                                                                                                                                                                                                                                                      USA
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RESULT 10
US-08-129-129-7
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JS-08-129-129-7
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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TELEX: 6714627CUSH
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HUGHES, Stephen Glyn
TITLE OF INVENTION: PLANT PROMOTER INVOLVED IN
TITLE OF INVENTION: CONTROLLING LIPID BIOSYNTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 8
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                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2015 base pair
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91303098.7
FILING DATE: 09-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 20:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                    FILING DATE: 08-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                             ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                             NAME/KEY:
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                                                                                                                                                                                                                                                                                     NAME: KOKULIS, Paul N. REGISTRATION NUMBER: 1
                                                                                                                          STRANDEDNESS:
                                                                                                          COPOLOGY:
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20005-3918
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nucleic acid
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1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                       (202) 822-0944
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Pred. No.
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US-08-972-927-1
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Вр
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Best Local Similarity
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                                                                                                                                      Matches
                                                                                                                                                                          Query Match
Best Local :
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,040
FILING DATE: 18-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/061,328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 831-494
INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:

PANITCH SCHWARZE JACOBS & NADEL, P.C.

ADDRESSEE: PANITCH SCHWARZE JACOBS Market Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 08-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Doyle Leary Ph.D.,
REGISTRATION NUMBER: 36,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
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   1259 GCTCTGATTGCTGCTGTG 1276
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                                                               2 GCTCTGATTCCTGCTCTG
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                                                                                                                                                                          Similarity
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Pennsylvania
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Lu, Yu-Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                    double
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88.9%;
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                                                                                                                                                                          88.9%;
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36,317
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                                                                                                                                   0;
                                                                                                                                      Score 14.8; D
Pred. No. 2.3e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.30
                                                                                                                                                                          .3e+02
                                                                                                                                                                                                             BB
                                                                                                                                                                                                      Length 5232;
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RESULT 12 US-08-194-468-1/c ; Sequence 1, Application US/08194468

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US-09-514-247A-7/c
; Sequence 7, Application US/09514247A
; Patent No. 6363361
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                APPLICANT: TRANSB SEIVAKU CO. LTD.
APPLICANT: TRANSB SEIVAKU CO. LTD.
APPLICANT: TRANSGUCHI, Tomoyasu
APPLICANT: MIZUKAMI, JUMKO
TITLB CHINVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PPA
FILE REFERENCE: TANIGUCHI=6
CURRENT STLING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: PCT/JP98/03734
PRIOR APPLICATION NUMBER: PCT/JP98/03734
PRIOR APPLICATION NUMBER: JP231084/1997
PRIOR APPLICATION NUMBER: JP231084/1997
PRIOR PILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VETSION 3.0
SBQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,468
FILING DATE: 10-FBB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (619)-546-9392
INFORMATION FOR SEQ ID NO: 1:
LENGTH: 7326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MONTMINY, MARC R.

TITLE OF INVENTION: ASSAYS FOR THE IDENTIFICATION OF

TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN

TITLE OF INVENTION: RESPONSIVE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 21,192
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16; Conserv
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88.9%; Pred. No. 2.3e+02;
tive 0; Mismatches
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, OTHER INFORMATION: n at position 1131 is unknown. US-09-514-247A-7
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US-08-961-739-1/c
                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-09-306-998-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-961-739-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 7326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09306998
Patent No. 6291173
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08961739A
Patent No. 6063583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                         SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/961,739A
CURRENT FILING DATE: 1997-10-31
EARLIER APPLICATION NUMBER: US 194,468
EARLIER FILING DATE: 1994-02-10
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Montminy, Marc R.
TITLE OF INVENTION: Methods for Treating Diabetes Mellitus
FILE REFERENCE: SALK1650-1
                                                                                                                        CURRENT APPLICATION NUMBER: US/09/306,998
CURRENT FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 60/084,740
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEO ID NOS: 72
                                                                                                                                                                                                                         APPLICANT: Bartel, Paul L.
APPLICANT: Tavttgian, Sean V.
TITLE OF INVENTION, MMSC2- An MMAC1 Interacting Protein
FILE REFERENCE: MMSC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: mouse
NAME/KEY: CDS
                                  ORGANISM: Homo sapiens
                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: n = A, T, C or G
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LOCATION: (1)...(7326)
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LOCATION: (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                     LENGTH: 7431
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Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14.8; DB 3;
Pred. No. 2.3e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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0

Search completed: June 21, 2003, 20:21:43 Job time : 65 secs 뭥 ; LOCATION: (57)..(6167) US-09-306-998-2 Query Match 77.9%; Score 14.8; DB 4; Length 7431; Best Local Similarity 88.9%; Pred. No. 2.4e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                   Score
       16.4
16.4
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Match Length
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19
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199.014 Million cell updates/sec
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AAH08486
ABK94976
AAH13643
AAH16697
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Lung carcinoma cDN
Lung carcinoma cDN
Human cDNA clone (
Human novel polynu
Human cDNA sequenc
Human cDNA sequenc
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Human cDNA encodin	AAS22683	22	6087	81.1	15.4	4 U	O
Drosophila melanog	ABL11003	23	4086	٠	15.4	44	a
	ABK35548	24	3995	81.1	Ü	43	
Human endometrial	ABK35489	24	3995	81.1	15.4	42	
Human nerve growth	ABA92502	24	3821	۲	15.4	41	
	AAD30143	24	3821		'n	40	
Human nerve growth	AAX34365	20	3821	ŗ	15.4	39	
Human secreted pro	ABA83332	22	1405	81.1	į'n	38	
Human secreted pro	AAV84549	20	1405	•	15.4	37	
Arabidopsis thalia	AAC34766	21	1336	•	15.4	36	C
~	AAC46183	21	1333	81.1	15.4	ω 5	a
Bovine-derived DNA	AAH21012	22	1267		ហ	ω 4	O
Nucleic acid G164c	AAV60020	19	1093	•	15.4	ω	Ω
Bovine embryonic g	ABN74153	24	975	81.1	5	32	
Human inflammatory	AAH92619	22	700	81.1	5	ω L	
Human musculoskele	AAL36191	22	322	•	5	30	a
Human schizophreni	AAS09301	22	319608	83.2	15.8	29	Ω
Human chromosome 1	AAH51601	21	319608		'n	28	Ω
Oesophagus cancer	ABL67703	24	302250		ū	27	
Hereditary haemoch	AAV57903	19	237326		'n	26	O
Hereditary haemoch	AAV57926	19	235033	83.2		25	O
Sorangium cellulos	AAA29349	21	71989			24	C
Human musculoskele	AAL35829	22	10126		•	23	ი
Human immune/haema	AAK75761	22	7180	83.2	15.8	22	O
Human full-length	AAK94355	22	2977	•	•	21	ი
Prostate cancer re	ABL69614	24	1391			20	O
ı benig	ABK64813	24	1391	٠		19	O
	ABN97245	24	1391			18	O
Zeaxanthin glycosy	AAQ13726	12	1200			17	Ω
\circ	ABN75155	24	227	•		16	
Human gene signatu	AAT24088	16	151	83.2	•	7	Ω
Human spliced tran	ABN45912	24	60			14	a
χυ Συ	ABQ88177	24	Ф	•		13	O
Human secreted pro	AAD05402	22	3185	•	•	12	O
secre	806	21	an.	•		11	
Human cDNA sequenc	AAS21273	22	1.0		16.4	10	

ALIGNMENTS

RESULT 1 AAX88558

AAX88558 standard; DNA; 19 BP

AAX88558;

10-SEP-1999

(first entry)

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Human chromosome 18q; mood disorder; polymorphic marker; detection; identification; trinucleotide repeat expansion; schizophrenia; anxiety disorder; adjustment disorder; personality disorder;
       WPI; 1999-418934/35.
                                                                                                                                                                                    nucleotide triplet repeat; ss.
                                                                                                                                                                                                                                      Human chromosome 18q YAC clone amplification primer
                           Del-Favero J, Raeymaekers P,
                                                                    18-DEC-1997;
                                                                                         17-DEC-1998;
                                                                                                              01-JUL-1999
                                                                                                                                  WO9932643-A2.
                                                                                                                                                                 Synthetic.
                                                 (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                                                                                                     Homo sapiens.
                                                                     97GB-0026804
                                                                                          98WO-EP08543
                            Van Broeckhoven
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RESULT 2
AAX88553/c
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S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (296.XX, 300.4, 311, 301, 13, 295.70), schizophrenia and related disorders (295, 297.1, 298.9, 297.3, 298.9), anxiety disorders (300.XX, 309.81, 308.3), adjustment disorders (309.XX) and personality disorders (codes 301.XX). Probes derived from genes associated with the mood disorder or related disorder can be used to detect pathological mutations or genetic variations in patients. The methods, probes and antibodies can be used to determine the susceptibility of an individual to a mood disorder or related disorder. The nucleic acids and proteins of the human gene can be used to treat mood disorders and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes detecting nucleotide triplet repeats in a region of human chromosome 18q disposed between polymorphic markers D18858 and D1885979 to identify a human gene associated with a mood disorder or related disorder. AAX88542 to AAX88705 represents human chromosome 18q YAC clones and primers corresponding to them, used in the exemplification of the present invention. YAC clones comprising a portion of the region of human chromosome 18q between markers D18958 and D1885979 are used to identify at least one human gene associated with a mood disorder or related disorder. The mood disorder or related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorder, is chosen from the Diagnostic and Statistical Manual of Mental Disorders, version 4 (DSM-IV) taxonomy. This includes mood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting nucleotide triplet repeats
                                                                                                                                                                                                                                                                                                                                                    anxiety disorder; adjustment disorder; personality disorder;
nucleotide triplet repeat; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX88553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX88553 standard; DNA; 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                           WPI; 1999-418934/35
                                                                                                                                                                                                       17-DEC-1998;
                                                                                                                                                                                                                                       01-JUL-1999
                                                                                                                                                                                                                                                                       WO9932643-A2
                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                   Human
             Claim
                                           Detecting nucleotide triplet repeats
                                                                                                                                                                         18-DEC-1997;
                                                                                                                                       (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG
                                                                                                                                                                                                                                                                                                                                                                                  iuman chromosome 18q; mood disorder; polymorphic marker; detec
identification; trinucleotide repeat expansion; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome 18q YAC clone nucleotide sequence #12.
             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCTCTGATTCCTGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCTCTGATTCCTGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig 15b;
          Fig 15a; 87pp; English
                                                                                                         ٩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 1 A; 7 C; 4 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                        Raeymaekers
                                                                                                                                                                       97GB-0026804.
                                                                                                                                                                                                       98WO-EP08543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                         'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                         Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                           Broeckhoven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in human chromosome 18q
                                             ij
                                             human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                   detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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CC The present invention describes detecting nucleotide triplet repeats in CC a region of human chromosome 18q disposed between polymorphic markers CC D18568 and D185979 to identify a human gene associated with a mood CC disorder or related disorder. AAX88542 to AAX8975 represents human CC chromosome 18q YAC clones and primers corresponding to them, used in the CC exemplification of the present invention. YAC clones comprising a CC portion of the region of human chromosome 18q between markers D18568 and CC D185979 are used to identify at least one human gene associated with a CC mood disorder or related disorder. The mood disorder or related CC D185979 are used to identify at least one human gene associated with a CC disorder, is chosen from the Disgnostic and Statistical Manual of Mental CC D1507ders (205. A) 311, 301, 13, 295.70), schizophrenia and related CC disorders (295, 297.1, 298.9, 297.3, 298.9), anxiety disorders (300.XX, CC disorders (295, 297.1, 298.9, 297.3, 298.9), anxiety disorders (200.XX, CC disorder or related disorder can be used to detect pathological motories and disorder or related disorder can be used to detect pathological reports and repairs or marketons or descriptions or canterior with an marketon marketons and marketons are described disorders in marketons to detect pathological
                                                                                                          mutations or genetic variations in patients. The methods, probes and antibodies can be used to determine the susceptibility of an individual to a mood disorder or related disorder. The nucleic acids and proteins of the human gene can be used to treat mood disorders and related
       Sequence
                                                                       disorders.
656 BP; 183 A; 165 C;
   208 G; 96 T; 4 other;
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Matches
                                     Best
                                           Query Match
                                     Local
533
                             19;
              Н
                                    Similarity
         CGCTCTGATTCCTGCTCTG 19
cecrcrearrecrecrers 515
                             Conservative
                                   100.0%;
                             0
                                    Score 19;
Pred. No.
                            Mismatches
                                     21;
                                            BB
                                            20;
                             0;
                                            Length
                             Indels
                                            656;
                             0:
                             Gaps
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ARRESULT 3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200228999-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA differentially expressed in granulocytic cells #138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK83567 standard; cDNA; 112460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease;
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Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity

Beazer-Barclay Y, Weissman

, MS

Yamaga ŝ

Vockley

Ç,

2002-435328/46

03-OCT-2000; 2000US-237189P 03-OCT-2001; 2001WO-US30821

(GENE-) GENE LOGIC

INC.

11-APR-2002

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RRSULT 4
AAF93539
ID AAF9
XX AAF9
AC AAF9
XX AAF9
XX AAF9
XX Lung
XX Huma
XX Huma
XX Huma
XX Huma
XX Homo
OS Homo
OS 10-F
XX WO20
XX Y
PF 21-J
XX 26-J
YA (GET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC GC, where differential expression of Gs is indicative of GCA.

CR Also included are modulating (M2) GA by contacting GC with an agent

CC that alters the expression of at least one gene in Gs; (2) screening

CR of an agent capable of modulating GGA or an inflammation (especially

CR chronic) in a tissue, an allergic response in a subject, exposure of a

CR subject to a pathogen or sterile inflammatory disease using the

CR chronic) in a tissue, an allergic response in a subject, exposure of a

CR subject to a pathogen or sterile inflammatory disease, by detecting the

CR chronic) in a tissue, an allergic response in a subject, exposure of a

CR subject to a pathogen or sterile inflammatory disease, by detecting the

CR chronic of expression in a sample of the tissue of gene (s) from Gs, where

CR the level of expression of the gene is indicative of inflammation;

CR distance of expression in a subject of a subject to a pathogen

CR or sterile inflammatory disease, by contacting a tissue having

CR inflammation with an agent that modulates the expression of gene (s)

CR preferably in an inflammation in a tissue; MR is useful for detecting GCA, MR is useful for

CR detecting an inflammation (especially chronic) in a tissue, an allergic

CR preferably in an inflammation in a tissue; MR is useful for

CR detecting an inflammation (especially chronic) in a tissue, an allergic

CR preferably in an inflammation in a tissue; MR is useful for

CR detecting an inflammation (especially chronic) in a tissue, an allergic

CR periodontal disease; also bacterial infection, viral infection,

CR periodontal disease; also bacterial infection, fungal infection and MS is

CR periodontal disease; also bacterial infection. The present

CR distinct infection with a parent did not form part

CR format directly from wipo at

CR formation for treating calls for the subjec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 112460 BP; 24087 A; 29523 C; 31203 G; 27647 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ
                                                     26-JUL-1999; 99US-0145701
                                                                                                                21-JUL-2000; 2000WO-US20006
                                                                                                                                                                                                                                       WO200107611-A2
                                                                                                                                                                                                                                                                                                                                                 Human; SRT; gene therapy; gene mapping; tissue typing; ss
                                                                                                                                                                                                                                                                                                                                                                                                               Lung carcinoma cDNA encoding SRT protein SEQ ID 360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF93539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF93539 standard; cDNA; 502
   (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88792 CTCTGATTCCTGCTCTG 88808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chip analysis
                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCTGATTCCTGCTCTG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as given in the specification, and comparin vel to an expression level in an unactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17; DB 24; Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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당 8

Sequence 502

BP;

94 A; 149 C; 119 G;

131

T; 9 other;

밁 8

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Sequences AAF93180 - AAF93743 represent polynucleotide sequences encoding human SRT proteins. The cDNA sequences are isolated from various different human tissue cDNA libraries. The invention relates to a method for detecting cDNA encoding an SRT protein, a vector containing cDNA encoding SRT, a host cell transformed with the vector, an isolated SRT polypeptide, and an antibody which binds to SRT. The polynucleotide sequence can be used in gene therapy and is useful in the recombinant production of SRT polypeptides, as a hybridisation probe to screen libraries to isolate cDNAs with sequence identity to SRT polypeptides, to map the gene encoding the SRT polypeptides and analysing genetic disorders, tissue typing and disease tissue detection. The SRT polymucleotide sequences can be used in polymerase chain reaction, screening for new therapeutic molecules and generation of antisense RNA and NNA.
                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid molecule encoding a SRT polypeptide is useful for production of recombinant SRT polypeptides, gene mapping, diagnosing genetic disorders and for gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                     Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-112729/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                     Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                     360; 663pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΨI
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RESULT 5 AAF93542 Query Match Best Local S Matches 01-FEB-2001 Human; SRT; gene therapy; gene mapping; tissue typing; ss. Lung carcinoma cDNA 26-JUL-1999; 21-JUL-2000; 2000WO-US20006. Homo sapiens, 21-MAY-2001 AAF93542; AAF93542 standard; cDNA; 511 WO200107611-A2 (GETH) GENENTECH 400 2 GCTCTGATTCCTGCTCTG 19 Similarity GCTCTGATTACTGCTCTG Conservative (first entry) 99US-0145701 INC. encoding 86.3%; 417 0; Score 16.4; DB 22 Pred. No. 3.2e+02; 0; Mismatches 1 SRT protein SEQ ID 363 ВP DB 22; Length 502; Indels 0; Gaps 0;

Sequences AAF93180 - AAF93743 represent polynucleotide sequences encoding human SRT proteins. The cDNA sequences are isolated from various

New isolated nucleic acid molecule encoding a SRT polypeptide for production of recombinant SRT polypeptides, gene mapping, diagnosing genetic disorders and for gene therapy -

is useful

WPI; 2001-112729/12.

Baker KP,

Goddard A,

Wood WI;

Claim 2; Fig 363; 663pp; English

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Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for detecting cDNA encoding an SRT protein, a vector containing cDNA encoding SRT, a host cell transformed with the vector, an isolated SRT polypeptide, and an antibody which binds to SRT. The polymicleotide sequence can be used in gene therapy and is useful in the recombinant production of SRT polypeptides, as a hybridisation probe to screen libraries to isolate cDNAs with sequence identity to SRT polypeptides, map the gene encoding the SRT polypeptides and analysing genetic disorders, tissue typing and disease tissue detection. The SRT polymucleotide sequences can be used in polymerase chain reaction, screening for new therapeutic molecules and generation of antisense RNA corrections.
                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                 Ota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH08486 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  different human tissue cDNA libraries. The invention relates to a method
to the complementary strand of a polynucleotide which comprises one the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combinate of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary
                                                                                      The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                      11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH08486;
                                                                                                                                                                                           and/or diagnosis of the
                                                                                                                                                                                                                                                                                                                              (HELI-)
                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-2000;
                                                                                                                                                                             full-length
                                                                                                                                                                                                                                                                                                                                                           JUN-
                                                                                                                                                                                                                                                                                               Ή
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445
                                                                                                                                                                                                                                                      2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                S
                                                                                                                                                  1; SEQ ID 5321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                            HELIX RES
                                                                                                                                                                                                                                                                                               Isogai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ecrcrearrecrecte 19
                                                                                                                                                                                                                                                                                Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone (5'-primer)
                                                                                                                                                                                                                                                                                                                                                      99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                        for synthesizing polynucleotides, particularly the 5602 cDNAs defined in the specification, and for the detection nosis of the abnormality of the proteins encoded by the
                                                                                                                                                                               CDNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 98
                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection; diagnosis; antisense
                                                                                                                                                                                                                                                                                Nishikawa
t T, Wakama
                                                                                                                                                                                                                                                                                                                            INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA; 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; 168 C; 119 G; 126 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.3%;
                                                                                                                                               2537pp + CD
                                                                                                                                                                                                                                                                                   Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3.200; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                搱
                                                                                                                                                                                                                                                                                               Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO:5321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                Hayashi K,
A, Nagai I
                                                                                                                                                ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.4;
No. 3.
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                                                                                                                                                                                                                                                                                  Saito K,
K, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                  Yamamoto T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                           where the
                                             combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 cDNA
~d SRT
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밁

S

Matches

Conservative

Mismatches

Indels

0;

Gaps

0

19 0;

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Query Match
Best Local
                                                                                                                                   polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03165 to AAH10742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                Sequence 857 BP; 196 A;
                                                                                                                       the present invention.
                        Similarity
                        94.4%;
                                                                                  235
                                                                                  Ç
                        Score 16.4;
Pred. No. 3
                                                                                  221
                                                                                  <u>و</u>
                                                                                    201
3.3e+02;
1;
                                             DB
                                                                                  H,
                                                                                    4 other;
                                         22;
                                         Length
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ABK94976
                                                                                                                                                                                                       RESULT
                                                                                                               Human novel
                                                                                                                                      30-AUG-2002
                                                                                                                                                                                 ABK94976
                                                                                                                                                                                                                                           141
                                                                                                                                                                                                                                                                N
infection.
                                                                                                                                                                                                                                             GCTCTGATTACTGCTCTG
                                                                                                                                                                                                                                                            GCTCTGATTCCTGCTCTG
         condition;
                                                                                                                                                                                  standard;
                                                                                                              polynucleotide #87.
                                                                                                                                      (first
                                                                                                                                                                                  cDNA; 1769
          thrombolysis; thrombosis; coagulation
                                                                                                                                                                                                                                             158
                                                                                                                                                                                    ВÞ
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Human; gene; ss; inflammatory condition; shock; sepsis; immune response; cancer; wound healing; central nervous system disease; haematopolesis; peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfusion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; Homo WO200244340-A2 allergic sapiens.

06-JUN-2002

30-NOV-2001; 2001WO-US47004.

30-NOV-2000; 2000US-0028952

(HYSE-) HYSEQ INC

Tang YT, Yamazaki ۷, Goodrich V, Ujwal ME, Liu C, Drmanac Zhou RT; ָש Asundi ۲, Wang Ġ Wang

ä

P-PSDB; 2002-508509/54. DB; ABG66752.

disorders, Novel nucleic acids and polypeptides for diagnosis, treatment inflammatory, autoimmune, nervous system, myeloid or lymphoid cancer and me, nervous system, mye promoting wound healing of cell

Claim 1; Page 546-548; 672pp; English

polypeptides. treating infla The invention ntion relates to human novel polynucleotides and associated ides. The polynucleotides and polypeptides are useful for inflammatory conditions such as arthritis, nephritis, Croh ischaemia-reperfusion injury, shock, sepsis, responses Crohn's

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RESULT 8
AAH13643/c
ID
AAH13643;
XX
AAH13643;
XX
AC
AAH13643;
XX
DT
26-JUN-2001 (first entry)
XX
DE
Human; primer; detection; diagno
XX
Human; primer; detection; diagno
XX
Homo sapiens.
XX
PN
EP1074617-A2.
XX
PN
C2-MAY-2000; 2000EP-0116126.
XX
PN
C2-MAY-2000; 2000JP-0183767.
PR
09-JUN-2000; 2000JP-018376.
PR
09-JUN-2000; 2000JP-018376.
PR
09-JUN-2000; 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, tissue repair, healing of burns, incisions, ulcers, treatment of osteoporosis, osteoarthritis, bone degenerative disorders and periodontal disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis and myasthenia gravis, allergic conditions such as asthma, thrombolysis or thrombosis and coagulation disorders. Sequences ABK94890-ABK94982 represent human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis. The sequences are involved in chemotractic or chemokinetic activity, regulation of haematopoiesis, treatment of myeloid or lymphoid cell disorders and platelet disorders such as thrombocytopenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain tissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA sequence SEQ ID NO:10485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1769 BP;
                                                                                                                Claim 8; SEQ ID 10485; 2537pp + CD ROM; English
                                                                                                                                                                                              Primer sets for synthesizing polynuclectides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                novel polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 GCTCTGATTACTGCTCTG
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17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
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       invention describes primer sets for synthesising cDNAs defined in the specification. Where a prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection; diagnosis; antisense therapy; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 A; 480 C; 483 G; 417 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          hikawa T,
Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashi K, S
ı A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saito K,
C, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1769;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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맑 8

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of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide comprises a sequence complementary to a complementary to a polynucleotide which comprises a 3'-end sequence, where the comprises a 3'-end sequence and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in comprises at least 15 nucleotides and the combination of the secification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, comparticularly full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH1362 and CDNAs easily without any specialised methods. AH03166 to AAH13632 compresent human amino acid sequences; and AAH13629 to AAH13632 compresent oligonucleotides, all of which are used in the exemplification of the compression of the compression of the comparation of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                          present
                                                                                                           invention.
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Sequence 1873 BP; 549 A; 419 Ç 526 G; 379 T; 0 other;

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Ś
                                    Query Match
Best Local :
                             Matches
              N
                                     Similarity
        GCTCTGATTCCTGCTCTG 19
                             Conservative
                                    86.3%;
94.4%;
897
                             0;
                                     Score 16.4;
Pred. No. 3
                              Mismatches
                                     .5e+02
                                            DB
                                            22;
                                            Length
                              Indels
                                            1873;
                             0;
                              Gaps
                              0;
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밁

914

GCTTTGATTCCTGCTCTG

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AAH16697
RESULT
                                                                                                                      Human; primer;
                                                                                                                              Human cDNA sequence SEQ ID NO:15859
                                                                                                                                               AAH16697;
                                                                                                       EP1074617-A2
                                                                                                                                      26-JUN-2001
                                                                                                                                                       AAH16697
                                                                                                              Homo sapiens
                                                                                                                                                      standard;
                                                                                                                                      (first
                                                                                                                       detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                      cDNA;
                                                                                                                                      entry)
                                                                                                                                                       2252
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28-JUL-2000; 2000EP-0116126. 07-FEB-2001.

27-AUG-1999; 99UP-0300253. 11-JAN-2000; 2000JP-0118776. 02-MAY-2000; 2000JP-0183767. 09-JUN-2000; 2000JP-0241899. 29-JUL-1999; (HELI-) HELIX RES 99JP-0248036. INST.

Ota T, ຸນ Isogai T, Nishikawa T, , Sugiyama T, Wakamats Wakamatsu Þ Hayashi K, Nagai ,7 Saito K, C, Otsuki ij

WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the **cDNAs**

Claim 8; SEQ ID 15859; 2537pp + CD ROM; English

sising 5602 1 primer set

The present invention describes primer sets for synthesising

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RESULT 10
AAS211
AC AAS21
AC AAS21
AC AAS21
AC AAS21
AC AAS21
AC AAS21
XX Unmar
XX Human
XX Human
XX Homo
XX H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human
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17; Conserv
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99WO-US30999.

99WO-US31243.

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2000WO-US00376.

2000WO-US03565.

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99WO-US30095.
99WO-US30911.
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Pred. No. 3
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RESULT 11
AAA80606
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Best Local (
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01-MAR-2000;
20-MAR-2000;
21-MAR-2000;
30-MAR-2000;
17-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith
Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic; antifheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000;
02-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2550 BP; 610 A;
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                                                                               Human
                                                                                                                                                                              AAA80606 standard; cDNA;
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DB; AAU12201.
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ME, Goddard A, Godd
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Stewart
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7 2000WO-US05601.
7 2000WO-US07377.
7 2000WO-US07532.
7 2000WO-US0439.
7 2000WO-US14042.
7 2000WO-US14042.
7 2000WO-US14941.
7 2000WO-US35264.
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                                                                                                                (first
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A, Godowski DJ, Gurney AL, Sh
Morenabe CK, Wood WI,
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                              591 T; 0 other;
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Zhang Z;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            multiple sclerosis; inflammatory disorder; inflammatory bowel disease; Crohn's disease; nephritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and/or diagnose various disease, disorders and conditions examples of which include: immune disorders e.g. Addison's disease, rheumatoid arthritts, dermatitis, and multiple sclerosis; inflammatory disorders e.g. inflammatory bowel disease, Crohn's disease and nephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                           hyperproliferative disorders such as paraproteinaemias and purpura; cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The proteins and polynucleotide sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene #1 and protein sequences are represented in sequences AAA80606 and AAB35576. Also given is an alternative protein product of human secreted protein gene #1 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Figure 1A-C; 803pp; English
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                                     17-JUL-2001
                                                                      AAD05402;
                                                                                                             AAD05402 standard; cDNA; 3185
                                                                                                                                                                                                                                                                                                                                                          Sequence 2609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to 12 secreted human proteins and to nucleotide sequences encoding them. The polynucleotide sequences in AAA80606-A80623 encode the 12 secreted protein sequences given
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                                                                                                                                                                                                                                                                                                    94.48;
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Pred. No. 3.
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immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; cardiovascular disorder; angiogenic disorder; skidney disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastrointestinal disorder; pregnancy-related disorder;
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cell culture; chemotaxis; food additive; chromosome 9;
                                                                                                                                                                                                                                                                                                                                   WPI; 2001-316490/33
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2000US-0215137.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Human
                                                                                                                                                                                                                                                                                                                                                      Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haematopoietic disorder;
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Nucleic acids encoding 29 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -

Claim <u>_</u> Page 423-424; 535pp; English.

amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 29 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, feetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis disbetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due t sunburn, to maintain organs before transplantation, for supporting cel culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be use as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, an AAD05389-AAD05473 represent cDNAs corresponding to 29 human secreted protein genes, and AAE01546-AAE01630 represent the proteins they encode. AAE01631-AAE01660 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the nt skin aging due to for supporting cell

Human secreted

protein-encoding gene

14 cDNA clone HPJBK11,

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                                                                                              osteoporosis or male osteoporosis, osteopenia, osteodystrophy, drug-induced abnormalities in bone formation or bone loss, conditions that involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis), skeletal disease linked to breast cancer, mastcocytosis, Fanconi syndrome or fibrous dysplasia. The present sequence is that of osteoblast differentiation associated cDNA marker of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of genes and their expression profiles associated with osteoblast differentiation for screening modulators bone formation, for diagnosi or treating e.g. osteoporosis, or as markers for the differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200250301-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-SEP-2002
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                                                 Note: The sequence data for this patent did not form part of t
specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                        (c) treating or monitoring treatment of the conditions cited in (b), or monitoring the progression of bone tissue deposition.

Specific conditions include postmenopausal osteoporosis, glucocorticoid
                                                                                                                                                                                                                                                                                                                                                                   (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
osteoblast formation or osteoporosis; or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2000; 2000US-255882P.
24-APR-2001; 2001US-285691P.
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                                                                                                                                                                                                                                                                                                                                                                                                                           osteoblasts,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (a) screening
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                       ftp.wipo.int/pub/published_pct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1515 GCTCAGATTCCTGCTCTG 1498
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteoblast; stem cell differentiation; bone tissue deposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROCTER & GAMBLE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENE LOGIC INC
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                                                                                                                                                                                                                                                                                                                                                                                                                        or bone tissue deposition;
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94.4%;
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    A). The present sequence represents a human
cDNA of the invention.

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Pred. No. 3.6e
0; Mismatches
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Best Local
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                                                                                                                                                                                                                messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcripted from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised minital transcriptomes. The libraries may also be used as specialised minital transcriptomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABN45912;
                                                                                                                                                 libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-257383/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shoshan A,
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02-MAY-2001; 2001US-287724P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABN45912
                            the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly fr
                                                                                           condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent
                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes oligonucleotide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID 18660; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmental-specific
                                                                                 oligonucleotide sequences from rats, humans and mice,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COMP-)
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94.4%;
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Pred. No. 4
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                                                                                                                                                                                                                                                                                      CC A single-stranded DNA (or its complementary strand or the corresp. CC double-stranded DNA) which comprises one of the 7837 "GS" sequences CC given in AAT1900.T26837 and which is able to hybridise to part of CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared CC from various human tissues; synthesis of cDNA was initiated from the CC all the 3'-oriented is unique to a particular mRNA species, almost call the 3'-oriented cDNAs hybridise with specific mRNAs. Each library CC is constructed so as to reflect accurately the relative abundance of CC different mRNAs in the particular tissue from which it was derived. CC The appearance frequency of a given GS in a cDNA library can be determined (egp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
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                                                                                                                                    Query Match 83.2%; Score 15.8; DB 16; Length 151; Best Local Similarity 89.5%; Pred. No. 5.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsubara K, Okubo K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-206931/27.
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                                                                                                                                                                                                                                   Sequence 151 BP; 49 A; 33 C; 39 G; 29 T; 1 other;
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Homo sapiens
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bassa 1 to 19)
Del-Favero,J., Raeymaekers,P. and Van Broeckhoven,C.
Mood disorder gene
Mood disorder gene
Patent: WO 9932643-A 14 01-JUL-1999;
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                            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 186351)

Hattori,M., Ishi,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 186,351 genomic DNA of 18q22

Published Only in DataBase (2000)

2 (Dases 1 to 186551)

2 (Dases 1 to 186551)

3 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mood disorder gene

Patent: MO 9932643-A 12 01-JUL-1999;

BROECKHOVEN CHRISTINE VAN (BE); DEL FAVERO JURGEN (BE); RAEYMAEKERS

PETER (BE); VLAAMS INTERUNIV INST BIOTECH (BE)

LOCATION/QUALIFIERS
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     Submitted
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates;
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/db_xref="taxon:9606"
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tive 0; Mismatches 0
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NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved 1 42519 contig of 42519 bp in length

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Sequence updated (26-May-2000).

* NOTE: This is a 'working draft' sequence. It currently * NOTE: This is a 'working draft' sequence of the pieces * consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is * ris not known and their order in this sequence record is * rins of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence.
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74497 74596: gap of 100 bp
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99677: gap of 100 bp
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* 145973 146072: gap of 10128 bp in length

* 146973 153170: contig of 7098 bp in length

* 153171 153270: gap of 100 bp

* 153271 156398: contig of 3128 bp in length

156399 156498: gap of 100 bp

156399 156498: gap of 100 bp

161724: contig of 5226 bp in length

161725 161824: gap of 100 bp
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110660 110759: gap of 100 bp
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87541. .99577
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74597. .87440
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146073. .153170
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165789. .169698
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115514. .124990
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/db_xref="taxon:9606"
/chromosome="18"
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AUTHORS
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Homo sapiens chromosome 18, clone RP11-793J2, comp.
AC009802
AC009802.13 GI:6705901
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 191395)
                                                                                                                                                                                                                                                                                                                                                Submitted (01-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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179198. .181636
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183745. .184761
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181737. .183644
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177404. .179097
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173655. .175764
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PRI 17-FEB-2000

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1 (Dases 1 to 191793)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 191,793 genomic DNA of 18q22

Published Only in DataBase (2000)

2 (Dases 1 to 191793)

2 (Dases 1 to 191793)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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Submitted (24-APR-2000) Masahira Hattori, The Institute of Physical submitted (24-APR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On May 30, 2000 this sequence version replaced gi:7649784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, 
Uapan: (B-mail:hattori@gsc.riken.go.jp, 
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, 
Fax:81-42-778-9924)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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sapiens chromosome 18 clone RP11-693A18
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27914. .27985
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26623. .26716
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100.0%; Pred. No. 20;
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177019 178822 contig of 1804 bp in length
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180178 181248 contig of 1855 bp in length
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1 17733 contig of 1873 bp in length
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1 10723: contig of 10723 bg in length
10724 10823: gap of 100 bp
10824 19450: contig of 8627 bp in length
19451 19550: gap of 100 bp
19551 28739: contig of 9189 bp in length
28740 28839: gap of 100 bp
28840 37796: contig of 9857 bp in length
37797 37896: gap of 100 bp
37897 45643: contig of 7747 bp in length
45644 45743: gap of 100 bp
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58 99276: contig of 3919 k
77 99376: gap of 100 bp
77 103751: contig of 4375 l
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11641: com-
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146311: contig of 2999
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132875: contig of
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161957: contig of 1522
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108407: contig of 4556 bp
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159: gap of 100 bp
86515: contig of 4356 bp in length
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                                                                                                                                                                                           1: gap of 100 bp
796: contig of 2062 bp
5: gap of 100 bp
731: contig of 1835 bp
1: gap of 100 bp
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2: contig of 2908
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9: contig of 4999
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5: contig of 2334
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contig of 3386 bp in length
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of 4321 bp in length
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Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grand, L.,
Galagan, J., Gardyna, S., Ginde, S., Heaford, A., Horton, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A
Howland, J. C., Iliev, I., Johnson, R., Landers, T., Leboozky, J.,
Klein, J., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
Levine, R., Lieu, C., Liu, G., Locke, K., McKernan, K., McPheeters, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 cecrcrearrecrectere 19
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* NOTE: This is a 'working draft' sequence. It currently 'consists of 4 contigs. The true order of the pieces 'is not known and their order in this sequence record is 'arbitrary. Gaps between the contigs are represented as 'runs of N, but the exact sizes of the gaps are unknown. 'This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 24, 2001 this sequence version replaced gi:13560423. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, W., Subrawanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McCarthy, M., McSwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Maylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., O'Neil, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Rogov, P., Rogov, P
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Collymore, A., Cooke, P., DeArellano, K., Dewar, Collymore, A., Cooke, P., Devar, Collymore, Co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sagiens chromosome 18, clone RP11-58983
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Homo sapiens chromosome 18 clone RP11-589E3 map 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Young,G., Zainoun,J., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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177019 178822: contig of 1804 bp
178823 178922: gap of 100 bp
                                                                                                                                                                                                                                                                       Center project name: L8567
Center clone name: 589_E_3
                                                                                                                                                                                                                                                                                                                                                   Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
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Collangelo,M., Collins,S.,
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K., Diaz, J.S

Karatas, A.,

Euteleostomi;

*** SEQUENCING

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2 (Danarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, J., Grand-Pierre, N., Gardyna, S., Ginde, S., Goyette, M., Graham, J., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., MacGaran, C., MacGaran, C., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, J., Mibova, T., Mlenga, V., Murphy, T., Naylor, J., Myuyen, C., Norbu, C., Norman, C.H., McMardy, T., Maylor, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Resta, R., Phunkhang, P., Pierre, N., Pollara, V., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Strauss, M., Travis, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Zembek, L., Zimmer, A., and Zody, M.
Direct, Sthmission
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Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 23, 2001 this sequence version replaced gi:13621272. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Homo sapiens chromosome 18 clone RP11-693A18 map 18, WORKING DRAFT
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Birren, B., Linton, L., Nusbaum, C. and Lander, B.
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                                                                                                                                             Direct Submission
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38369 109704: contig of 71336 bp in length
109705 109804: gap of 100 bp
109805 128704: contig of 18900 bp in length
128705 128804: gap of 100 bp
128805 198291: contig of 69487 bp in length.
Location/Qualifiers
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|db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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* consists of 8 contigs. The true order of the pieces 
* is not known and their order in this sequence record is
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45184 45283: gap of 100 bp
45284 46768: contig of 1485 bp in length
46769 46866: gap of 100 bp
46869 47961: contig of 1093 bp in length
47962 48061: gap of 100 bp
48062 49643: contig of 1582 bp in length
49644 49743: gap of 100 bp
49744 51393: contig of 1650 bp in length
51394 51493: gap of 100 bp
51494 74531: gap of 100 bp
51494 74531: gap of 100 bp
74532 74631: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality coverage: 11.3 in Q20 bases; agarose-fp Quality coverage: 10.9 in Q20 bases; sum-of-contigs
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Center clone name: 693 A 18
----- Summary Statistics
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Center: Whitehead Institute/ MIT Center for Genome Research
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27811 201734: contig of 73924 bp in length
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clone_end:SP6
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                                                                                                                               'note="assembly_fragment'
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                                                                          18;
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Interaction of dishevelled and Xenopus axin-related protein required for wnt signal transduction
MOJ. Cell. Biol. 20 (6), 2228-2238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-APR-1999) Microbiology and Medical Genetics, Harvard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antipova, A., Itoh, K. and Sokol, S. Direct Submission
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                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           School, BIDMC, East Campus, RW663, 330 Brookline Avenue, MA 02215, USA Location/Qualifiers
                                                                                                                                                                     EVSEEDAVLPLFEEKIICKVERAC"
501 c 507 g 476 t
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AKLMKKHHRETASVTPCPELKKATHRAASQPAHLFLQDTSMPPLTAPNTLDQLEEARR
RLVEDKRVPKLHKSRCVQSTTLKEKGKTAESVPSSGESTLKLSEEQKTAKKPSSECPG
                                                                                                                                                                                                                                                                                 LHHFSSGMGKINRAFSRIPPRNQRSHFRKLEQTYQYFAPAASINDSEISDALTEDSM
SMTDGSVDGIPPYRSKQREIHRSVSANGKVSLPFVPRTMRPAADHDSPSSTADL
TIALEKVIKQRAEKLESKLQRIKEEREITAPVIPERSSHETVPQAALEDDPQSILDD
HVSRVLKTPANLSPRSQSPFVQRKGKFQPAFSKGQTSTSCHLRPKVPQGMEATSTLAS
                                                                                                                                                                                                                                                                                                                                                            HLKHKEDFNREAEGCVAHDSRFSRWGRSLAILLIDDQDGATLFRWYLEGEGLGDLLTFW
FACNGFRAMDFLEPKTSKTAKAIYRWYVQNSSAVSGRLKPTTRTQVKECVKNHQLNKT
VFDQAQQEIQRAMEQEAFTSFLQSDICKEYARGVEDSPTPESPGPGLPTLTEDEEFGG
                                                                                                                                                                                                           QGLAIVYYFCGERIPYMIRTKEPSLTLQEFKELLSKKGSNKYYFKKESHEFECNAVFÇ
                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="axin-related protein"
/protein_id="AAF22574.1"
/db_xref="GI:6652991"
                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MSSAGVLTCIPDSGPIFRETSLRPPVPGQETNNFKPEKFTMDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="ARP"
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                                                                        Score 17.4; D
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                                                                                                              DB 5;
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RESULT 9

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                                                                                                                                                                                                                                                                     HTG; HTGS PHASE1.
Rattus norvegicus.
Rattus norvegicus
Eukaryota; Metazoa;
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Davila,M.L., Davis,C., Davy-Carrott, Ding,Y., Dinh,H.H., Delamey,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,K.J., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Douthwaite,K.J., Draper,H., Dugan-Rocha,J., Escotto,M., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Falls,T., Garza,N., Gill,R.,
                                                                                                                                                                                                                                                                                                                                                 151395 bp D
Rattus norvegicus clone CH230-43707,
***, 62 unordered pieces.
AC128860
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HTG.
                                                                          Center: Washington University Genome Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (16-JUL-2002) Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McPherson, J.D. and Waterston, R.H. The sequence of Mus musculus clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: M_BB0535L06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site:http://genome.wustl.edu/gsc/index.shtml
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McPherson, J.D. and Wat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTCTGATTCCTGCTCTG 99806
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/db_xref="taxon:10090"

/clone="RP24-535L6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
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7, *** SEQUENCING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 62 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                            be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: Plasmid; Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 88196 bases at least Q40 Consensus quality: 94027 bases at least Q30 Consensus quality: 97692 bases at least Q20
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Web site: http://
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Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buthay, C., Burch, P., Burkett, C., Burcell, K.L., Byrd, M.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davy-Carnoll, L., Dederich, D.A., Davis, C., Davy-Carnoll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, M., Ford, J., Foster, P., Frantz, P., Falls, T., Garza, W., Ganrartne, P., Hale, S., Hamilton, K., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hallyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kratovic, J., Kueshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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***, 74 unordered pieces.
AC119463
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Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen,
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Worley,K.C.
Direct Submission
Submitted (27-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 168369)
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Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Mabua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,E., Mitchell,T., Mohabat,K., Morgan,M., Morris,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of Molecular and Human
Baylor Plaza, Houston,
On Jul 14, 2002 this se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of re Assembly program: Phrap; version 0.990329
Consensus quality: 104715 bases at least Q40
Consensus quality: 111142 bases at least Q30
Consensus quality: 116085 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: GUTZ
Center clone name: CH230-:
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence NOTE: Estimated insert size may differ from sequence length (see http://www.lgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is as soon as it be preserved. 1053 1153 2489 2589 2589 4102 4202 5284 5284 6394 6394 6394 6493: 4101: 1052: contig is available and the accession number will gap of contig ĝ unknown
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                                                                                       Center:Beijing Center
Center code:Beijing Center
Center code:Beijing Center
Center code:Beijing
Website:http://hgc.igtp.ac.cn
http://www.genomics.org.cn
Contact:hgc@igtp.ac.cn.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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                                                                                                                                                                                                                                                                                          Submitted (03-FEB-2000) Genomic Dept., Chinese National Human Genome Center at Shanghai, 315 Guo Shou Jing Road, Shanghai, Shanghai 201203, P. R. China On Sep 26, 2000 this sequence version replaced gi:6862623.
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 176054)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC022377.2 GI:10305054
HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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36597: 37636: 37736: 39316:

unknown of 1580 unknown of 1039

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gap of contig gap of contig gap of gap of contig

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of 1023

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unknown

32820: 32920: 29240: 30671: 28082: 29140: 26864: 27982:

gap of contig gap of contig gap of contig gap of contig

of 1485 unknown

length

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unknown of 2049 unknown of 1431

length bp in length

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length bp in]

length

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length
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length bp in length

20984 220499 222149 222149 233997 253557 25457 26467 26467 27983 27983 27983 27983 27983 27973 27973 27973 27973 27973 27974 27973 2

23896 23996

gap of contig gap of contig

of 1360

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22048 20883: 17806: 19352:

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14056 15938 16038 17707 177807 17807 19353 19453 20884

19452:

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gap of contig gap of contig

of 1598 unknown

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length

length

9703 9803 11138 11238 11238

gap of contig gap of contig

length bp in :

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length

Length

48721 46011: 47510: 45911 44694

of 1111

length bp in 1

length

unknown

2101

n length
l bp in length
n length
l bp in length

gap of contig

of 1499 unknown unknown of 1775 of 1051 unknown

length
by in length
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length
by in length

gap of contig gap of contig gap of contig

of 1217

44594

42819

unknown

length bp in length bp in

length length length

55637: 57248: 57348: 59510: 59610:

unknown of 2162 of 1611

gap of contig

n length
1 bp in length
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gap of contig gap of contig gap of contig gap of contig

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gap of contig gap of

unknown of 1508 unknown

n length
s in length
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by in length
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54084: 54184:

gap of contig gap of contig

of 1353 unknown of 1751 gap of contig gap of contig gap of contig

unknown of 1211

unknown

ORIGIN

Locus

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SOURCE
ORGANISM
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AC018831/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
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Best Local
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100101, P.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zeng, Y., Hu, S., Dong, W., Wang, J., Zhang, Y., Zhang, H., Liu, B., Bao, W., Sun, Y., Wu, Q., Wang, H., Yang, X., Cheng, C., Wang, Y., Niu, Y., Qi, X., Li, T., Zhang, H., Liu, N., Wu, D., Yu, B., Fan, H., Liu, Y., Li, G., Li, C., Bao, Q., Bao, J., Wang, X., Song, L., Zhang, L., Guo, D., Huang, F., Zhang, G., Li, J., Bian, X., Zhang, M., Li, L., Feng, X., Wang, X., Yu, J. and Yang, H. Bian, X., Zhang, M., Li, L., Feng, X., Direct Submitsion
Submitted (21-DEC-1999) Human Genetics, Datun Road, Beijing, Beijing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, M., Li, C., Li, V., Liu, N., Liu, N., Liu, B., Liu, Y., Li, W., Li, W., Li, V., Luo, C., Luo, J., Niu, Y., Qi, Q., Qi, X., Song, L., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, J., Wang, J., Wang, J., Wang, J., Wang, J., Wang, Y., Wang, Y., Wang, X., Wang, Y., Wu, D., Wang, L., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zeng, Y., Zhang, G., Zhang, H., Zhang, H., Zhang, M., Zhang, X., Zhang, Y., Zhan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC018831.4 GI:12718884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chromosome 3p genomic sequence Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li,F., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 178548)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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/db_xref="taxon:9606"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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47246 c 47642 g 41071 t
    (09-FEB-2001)
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; Pred. No. 1.5e-
0; Mismatches
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Human Genomic Center, Institute of
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AUTHORS
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AC125748
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CE 1 (Dases 1 to 189040)

1 (Dases 1 to 189040)

RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Blabaria, J., Benton, J., Blanage, K., Blankenburg, K., Bonnin, D., Burbaria, J., Benton, J., Blanage, K., Blankenburg, K., Bonnin, D., Bunket, C., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T. F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Darthart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garca, N., Gill, R., Gorrell, J.H., Goverar, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, J., Hernandez, J., Hollins, B.,
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Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 182029 bases at least Q40
Consensus quality: 182113 bases at least Q30
Consensus quality: 182119 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
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Quality coverage: 15.40x in Q20 bases; sum-of-contigs
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http://www.genomics.org.cn
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18; Conservative
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Pred. No. 1.5e+02;
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Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, W., Ieal, B., Lewis, L.C., Lewis, L. Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Mall, D., Newtson, J., Newtson, W., Worgan, M., Morris, S., Moser, M., Neal, D., Newtson, W., Newtson, M., Okwonu, G., Oragunye, N., Oriedo, R., Pace, A., Payton, B., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scheret, S., Scott, G., Shen, H., Shoshkari, N., Sisson, I., Sodergren, E., Sonake, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, M., Thomas, S., Ward-Moore, S., Warren, R., Washington, C., Watlianson, S., Warren, R., Washington, C., Watlington, S., Warlow, S., and Gibbs, R., Lupublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (14-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 2, 2002 this sequence version replaced gi:21630324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (30-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 189040)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 58 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 143305 bases at least Q40
Consensus quality: 148956 bases at least Q30
Consensus quality: 153138 bases at least Q20
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-helpebcm.tmc.edu
Contact: hgsc-helpebcm.tmc.edu
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Center clone name: CH230-11K12
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2751: contig
2851: gap of
3991: contig
4091: gap of
4091: gap of
5820: contig
5920: gap of
7103: contig
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23405: gap of
24720: contig
24820: gap of
26732: contig
26832: gap of
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9673: gap of
11149: contig
11249: gap of
12583: gap of
13764: contig
12683: gap of
13764: contig
116139: contig
116139: contig
11629: gap of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL845471 192180 bp DNA linear HTG 17-AUG-2002 Mus musculus chromosome 2 clone RP23-320N1, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.
                                                                                                                                                                                                                                                                      Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 21, 2002 this sequence version replaced gi:22265699.
                               coverage: 5.63x in Q20 bases; agarose-fp
                                                                                                                                                                                        Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                   Web. site:
                                                                                                                                                                                                                                    Center code: SC
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1.
                                                                                                                                                                          Center project name: bM320N1
                                                                                                                                                                                                                                              Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                     Plumb,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL845471.2 GI:22416270
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NOTE: This is a 'working draft' sequence. It currently
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Pred. No. 1.
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of 4158
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                                           sum-of-contigs Quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146227 146326: gap of 100 bp
146327 159656: contig of 1330 bp in length
159657 159756: gap of 100 bp
159757 192180: contig of 32424 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 bp
131700: contig of 7338 bp
131701 131800: gap of 100 bp
131801 146226; contin of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 4890: contig of 4890 bp in length

4891 4990: gap of 100 bp

4991 33912: contig of 28922 bp in length

33913 34012: gap of 100 bp

34013 43204: contig of 9192 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43205 43304: gap of 100 bp 43305 104293: contig of 60989 bp in length
                                                                                                                                                                       /note="assembly_fragment:00228
fragment_chain:1"
114335. .124262
/note="assembly_fragment:00046
fragment_chain:1"
159757. .192180
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                                                                      note="assembly_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="RP23-320N1"
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1111164: contig of 4084 bp in length
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                                           .159656
                                                       ssembly_fragment:00101
_chain:1"
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_chain:1"
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                                                                                                                                                                                                                                                                           ssembly_fragment:02089
_chain:1"
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contig of 2970 bp
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RESULT 15 AL845471 LOCUS

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Matches

REFERENCE

AUTHORS

JOURNAL

COMMENT

ORGANISM

KEYWORDS ACCESSION DEFINITION

VERSION